

Antibiotic susceptibility and genetic relatedness of *Shigella* species isolated from food and human stool samples in Qazvin, Iran

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Abstract

Objective: The aim of this study was to investigate the genetic relatedness and antimicrobial resistance among *Shigella* species isolated from food and stool samples. Using cross sectional study method, *Shigella* spp. were isolated from food and clinical samples using culture-based, biochemical and serological methods. Antimicrobial susceptibility and genetic relatedness among the isolates were evaluated using disk diffusion and RAPD-PCR methods respectively. **Results:** The prevalence of *Shigella* spp. were 4.84 and 7.7% in food and stool samples respectively. All food isolates were *Sh. sonnei*. 91.42% of the *Shigella* stool isolates were *Sh. sonnei*. 62.5% of food isolates were resistant to tetracycline. 46.8, 50 and 65.8% of clinical isolates were resistant to imipenem, amikacin and azithromycin respectively. 50 and 85.7% of the food and clinical isolates respectively were MDR. Dendrogram generated by RAPD-PCR showed that the isolates from food and stool samples were categorized in a same group. Close genetic relatedness between MDR *Shigella* isolates from food and clinical samples indicate that foods can be considered as one of the main vehicles for transmission of MDR *Shigella* to human causing acute diseases. Survey of MDR *Shigella* among food and clinical samples is strongly suggested to be implemented. © 2021, The Author(s).

Author keywords

Antimicrobial susceptibility; Food samples; Genetic relatedness; *Shigella* species; Stool specimens